RAW SEQUENCE LISTING
ERROR REPORT

SEP 1 6 2002

The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) detected errors when processing the following computer readable form:

Application Serial Number: _10/007,621_

Source: _OIPE_

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THE ATTACHED PRINTOUT EXPLAINS DETECTED ERRORS.
PLEASE FORWARD THIS INFORMATION TO THE APPLICANT BY EITHER:
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2) TELEPHONING APPLICANT AND FAXING A COPY OF THIS PRINTOUT, WITH A NOTICE TO COMPLY
FOR CRF SUBMISSION QUESTIONS, PLEASE CONTACT MARK SPENCER, 703-308-4212.

FOR SEQUENCE RULES INTERPRETATION, PLEASE CONTACT ROBERT WAX, 703-308-4216.
PATENTIN 2.1 e-mail help: patin21help@uspto.gov or phone 703-306-4119 (R. Wax)
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TO REDUCE ERRORED SEQUENCE LISTINGS, PLEASE USE THE **CHECKER VERSION 3.1 PROGRAM**, ACCESSIBLE THROUGH THE U.S. PATENT AND TRADEMARK OFFICE WEBSITE. SEE BELOW FOR ADDRESS:
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Applicants submitting genetic sequence information electronically on diskette or CD-Rom should be aware that there is a possibility that the disk/CD-Rom may have been affected by treatment given to all incoming mail.
Please consider using alternate methods of submission for the disk/CD-Rom or replacement disk/CD-Rom.
Any reply including a sequence listing in electronic form should NOT be sent to the 20231 zip code address for the United States Patent and Trademark Office, and instead should be sent via the following to the indicated addresses:

1. EFS-Bio (<http://www.uspto.gov/ebc/efs/downloads/documents.htm> , EFS Submission User Manual - ePAVE)
2. **U.S. Postal Service:** U.S. Patent and Trademark Office, Box Sequence, P.O. Box 2327, Arlington, VA 22202
3. **Hand Carry directly to:**
   U.S. Patent and Trademark Office, Technology Center 1600, Reception Area, 7th Floor, Examiner Name, Sequence Information, Crystal Mall One, 1911 South Clark Street, Arlington, VA 22202
           Or
   U.S. Patent and Trademark Office, Box Sequence, Customer Window, Lobby, Room 1B03, Crystal Plaza Two, 2011 South Clark Place, Arlington, VA 22202
4. **Federal Express, United Parcel Service, or other delivery service to:** U.S. Patent and Trademark Office, Box Sequence, Room 1B03-Mailroom, Crystal Plaza Two, 2011 South Clark Place, Arlington, VA 22202

Revised 01/29/2002

ERROR DETECTED   **SUGGESTED CORRECTION**   SERIAL NUMBER: *10/007,621*

ATTN: NEW RULES CASES: PLEASE DISREGARD ENGLISH "ALPHA" HEADERS, WHICH WERE INSERTED BY PTO SOFTWARE

1_____Wrapped Nucleics   The number/text at the end of each line "wrapped" down to the next line. This may occur if your file
       Wrapped Aminos   was retrieved in a word processor after creating it. Please adjust your right margin to .3; this will
                               prevent "wrapping."

2_____Invalid Line Length   The rules require that a line not exceed 72 characters in length. This includes white spaces.

3_____Misaligned Amino   The numbering under each 5th amino acid is misaligned. Do not use tab codes between numbers;
       Numbering   use space characters, instead.

4_____Non-ASCII   The submitted file was not saved in ASCII(DOS) text, as required by the Sequence Rules. Please
                             ensure your subsequent submission is saved in ASCII text.

5_____Variable Length   Sequence(s)____contain n's or Xaa's representing more than one residue. Per Sequence Rules,
                             each n or Xaa can only represent a single residue. Please present the maximum number of each
                             residue having variable length and indicate in the <220>-<223> section that some may be missing.

6_____PatentIn 2.0   A "bug" in PatentIn version 2.0 has caused the <220>-<223> section to be missing from amino acid
       "bug"   sequences(s) _____. Normally, PatentIn would automatically generate this section from the
                             previously coded nucleic acid sequence. Please manually copy the relevant <220>-<223> section to
                             the subsequent amino acid sequence. **This applies to the mandatory <220>-<223> sections for**
                             Artificial or Unknown sequences.

7_____Skipped Sequences   Sequence(s) _____ missing. If intentional, please insert the following lines for each skipped sequence:
       (OLD RULES)   (2) INFORMATION FOR SEQ ID NO:X: (insert SEQ ID NO where "X" is shown)
                             (i)   SEQUENCE CHARACTERISTICS: (Do not insert any subheadings under this heading)
                             (xi) SEQUENCE DESCRIPTION:SEQ ID NO:X: (insert SEQ ID NO where "X" is shown)
                             This sequence is intentionally skipped

                             Please also adjust the "(ii) NUMBER OF SEQUENCES:" response to include the skipped sequences.

8_____Skipped Sequences   Sequence(s) _____ missing. If intentional, please insert the following lines for each skipped sequence.
       (NEW RULES)   <210> sequence id number
                             <400> sequence id number
                             000

9_____Use of n's or Xaa's   Use of n's and/or Xaa's have been detected in the Sequence Listing.
       (NEW RULES)   Per 1.823 of Sequence Rules, use of <220>-<223> is MANDATORY if n's or Xaa's are present.
                             In <220> to <223> section, please explain location of n or Xaa, and which residue n or Xaa represents.

10_____Invalid <213>   Per 1.823 of Sequence Rules, the only valid <213> responses are: Unknown, Artificial Sequence, or
       Response   scientific name (Genus/species). <220>-<223> section is required when <213> response is Unknown or
                             is Artificial Sequence

11_____Use of <220>   Sequence(s) _____ missing the <220> "Feature" and associated numeric identifiers and responses.
                             Use of <220> to <223> is MANDATORY if <213> "Organism" response is "Artificial Sequence" or
                             "Unknown." Please explain source of genetic material in <220> to <223> section.
                             (See "Federal Register," 06/01/1998, Vol. 63, No. 104, pp. 29631-32)   (Sec. 1.823 of Sequence Rules)

12_____PatentIn 2.0   Please do not use "Copy to Disk" function of PatentIn version 2.0. This causes a corrupted file,
       "bug"   resulting in missing mandatory numeric identifiers and responses (as indicated on raw sequence
                             listing). Instead, please use "File Manager" or any other manual means to copy file to floppy disk.

13_____Misuse of n   n can only be used to represent a single nucleotide in a nucleic acid sequence. N is not used to represent
                             any value not specifically a nucleotide.

IN THE UNITED STATES PATENT AND TRADEMARK OFFICE

APPLICANTS: Hardin et al. § ART UNIT NO.: 1645
SERIAL NO.: **10/007,621** § EXAMINER: UNKNOWN
FILED: 12/03/01 § DOCKET NO.:00007/02UTL
§
TITLE: Enzymatic Nucleic Acid Synthesis: §
Compositions and Methods for Altering §
Monomer Incorporation Fidelity §

STATEMENT REGARDING SUBSTITUTE PAPER COPY OF SEQUENCE LISTING AND CRF COPY OF SEQUENCE LISTING

Dear Sir/Madam:

In response to a Notice to Comply with Sequence Rules, Applicant used the PatentIn 3.1 software for the United States Patent and Trademark Office to generate a hard copy and electronic copy of the sequence listing as required by the Notice.
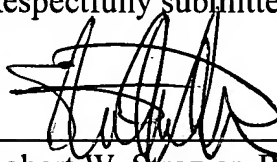
Applicants' Attorney verifies that the paper and electronic listing are identical, both generated by PatentIn 3.1.

Applicants' Attorney has attempted in good faith to respond to this notice; however, Applicants' Attorney must point out that at numerous part of the specification, reference is made to specific enzymes and DNA molecules, without the actual sequence. Applicants did not include actual sequences because the actual sequences are not germane to this application. The application relates to functionalized dNTPs or other small molecules that increase base incorporation fidelity. The invention is not related to any specific nucleic acid sequence or peptide sequence.

If this submission is considered deficient, please have someone from the sequence compliance group call me. I have attempted several times to get an answer on the issue of whether a nucleic acid or peptide sequence listing is required for a mere reference to a specific nucleic acid molecule or a specific enzyme or polypeptide, without sequence listing, in an application.

Applicant's attorney has corrected a defect in the earlier submission. Sequence No. 2 was a repeat of Sequence No. 1 in the earlier submission and has been corrected in this submission to be identical to the sequence set forth on Page 59 of the Specification. The mistake was unintended and merely left out one primer sequence and duplicated another.

Respectfully submitted,

Date: **13 September 2002**

Robert W. Strozier, Reg. No. 34,024
Attorney for Applicants